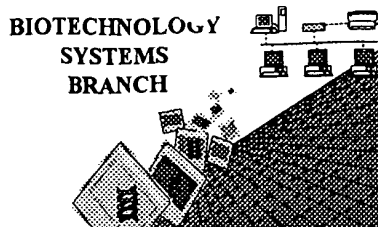


504/1



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/031818
Source: P5/10
Date Processed by STIC: 2/13/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/03/818

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ **Misaligned Amino
Numbering** The numbering under each 3rd amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(ii) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ **Use of <220>** Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n** n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



PCT10

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/031,818

DATE: 02/13/2002
TIME: 08:48:59

Input Set : A:\EP.txt
Output Set : N:\CRF3\02132002\J031818.raw

Does Not Comply
Corrected Diskette Needed

pp 1-2

delete duplicate <110>
<110> is shown once only

W--> 2 <110> APPLICANT: OZEKI, Yoshihiro
W--> 3 ~~<110>~~ APPLICANT: SAN-EI GEN F.F.I., INC.,
W--> 4 <120> TITLE OF INVENTION: NOVEL MINIATURE INVERTED-REPEAT TRANSPOSABLE ELEMENTS (MITES)-LIKE
W--> 5 ELEMENT AND TRANSCRIPTIONAL ACTIVATION ELEMENT
W--> 6 <130> FILE REFERENCE: P00-14
C--> 7 <140> CURRENT APPLICATION NUMBER: US/10/031,818
C--> 7 <141> CURRENT FILING DATE: 2002-01-17
7 <150> PRIOR APPLICATION NUMBER: JP 1999/206316
8 <151> PRIOR FILING DATE: 1999-07-21
9 <150> PRIOR APPLICATION NUMBER: JP 1999/206320
10 <151> PRIOR FILING DATE: 1999-07-21
11 <150> PRIOR APPLICATION NUMBER: JP 2000/175825
12 <151> PRIOR FILING DATE: 2000-06-12
W--> 13 <160> NUMBER OF SEQ ID: 14

ERRORED SEQUENCES

71 <210> SEQ ID NO: 4
72 <211> LENGTH: 8
73 <212> TYPE: DNA
74 <213> ORGANISM: Carrot (Daucus carota L.cv.Kurodagosun)
W--> 75 <400> SEQUENCE: 4
E--> 76 gttgcaaa 8 (global format error) see item 1 on Error Summary sheet
77 8
79 <210> SEQ ID NO: 5
80 <211> LENGTH: 8
81 <212> TYPE: DNA
82 <213> ORGANISM: Carrot (Daucus carota L.cv.Kurodagosun)
W--> 83 <400> SEQUENCE: 5
E--> 84 gttgcaac 8 item 1
85 8
87 <210> SEQ ID NO: 6
88 <211> LENGTH: 8
89 <212> TYPE: DNA
90 <213> ORGANISM: Carrot (Daucus carota L.cv.Kurodagosun)
W--> 91 <400> SEQUENCE: 6
E--> 92 tttgcaaa see item 1
93 8
95 <210> SEQ ID NO: 7
96 <211> LENGTH: 8
97 <212> TYPE: DNA
98 <213> ORGANISM: Carrot (Daucus carota L.cv.Kurodagosun)

RAW SEQUENCE LISTING

DATE: 02/13/2002

PATENT APPLICATION: US/10/031,818

TIME: 08:48:59

Input Set : A:\EP.txt

Output Set: N:\CRF3\02132002\J031818.raw

W--> 99 <400> SEQUENCE: 7 *Item 1*
E--> 100 ttgcaac
101 8
103 <210> SEQ ID NO: 8
104 <211> LENGTH: 7
105 <212> TYPE: DNA
106 <213> ORGANISM: Carrot (Daucus carota L.cv.Kurodagosun)

W--> 107 <400> SEQUENCE: 8 *Item 1*
E--> 108 tatgcaa
109 7
111 <210> SEQ ID NO: 9
112 <211> LENGTH: 7
113 <212> TYPE: DNA
114 <213> ORGANISM: Carrot (Daucus carota L.cv.Kurodagosun)

W--> 115 <400> SEQUENCE: 9 *Item 1*
E--> 116 aatgcaa
117 7
119 <210> SEQ ID NO: 10
120 <211> LENGTH: 158
121 <212> TYPE: DNA
122 <213> ORGANISM: Carrot (Daucus carota L.cv.Kurodagosun)

W--> 123 <400> SEQUENCE: 10
124 gggatctttt taaaaatacc catctgtaaa attatTTTTT taaaaatact accatctttt 60
125 tcattgtttt taaaaatacc ttttcataaa tttttttttt caaaaatagc atttgcaact 120
E--> 126 ttgcaacct catttgcaac cttgggcggc gcagccgt 158
127 158
129 <210> SEQ ID NO: 11
130 <211> LENGTH: 158
131 <212> TYPE: DNA
132 <213> ORGANISM: Carrot (Daucus carota L.cv.Kurodagosun)

W--> 133 <400> SEQUENCE: 11
134 acggctggcg ccgcctgtag ttgcaaatga ggttgcaaaa gttgcaaaca gtatttttga 60
135 aaaaaagatt ttatgaaaag gtatttttaa aaataattct ggaaggtagt atttttgaaa 120
E--> 136 acaataaaag aaaaggtagg tagttttgta gatttccc *same even*
137 158
139 <210> SEQ ID NO: 12
140 <211> LENGTH: 32
141 <212> TYPE: DNA
142 <213> ORGANISM: Carrot (Daucus carota L.cv.Kurodagosun)

W--> 143 <400> SEQUENCE: 12
E--> 144 ctccctacgt cccattttat gtgacctcat tt 32
145 32
147 <210> SEQ ID NO: 13
148 <211> LENGTH: 32
149 <212> TYPE: DNA
150 <213> ORGANISM: Carrot (Daucus carota L.cv.Kurodagosun)

W--> 151 <400> SEQUENCE: 13
E--> 152 aaactcattc acataaaatg ggacagaggg ag 32
153 32

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/031,818

DATE: 02/13/2002

TIME: 08:49:00

Input Set : A:\EP.txt

Output Set: N:\CRF3\02132002\J031818.raw

L:3 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:6 M:283 W: Missing Blank Line separator, <130> field identifier
L:7 M:270 C: Current Application Number differs, Replaced Current Application No
L:7 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:13 M:283 W: Missing Blank Line separator, <160> field identifier
L:19 M:283 W: Missing Blank Line separator, <400> field identifier
L:38 M:283 W: Missing Blank Line separator, <400> field identifier
L:49 M:283 W: Missing Blank Line separator, <400> field identifier
L:75 M:283 W: Missing Blank Line separator, <400> field identifier
L:76 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:8 SEQ:4
L:83 M:283 W: Missing Blank Line separator, <400> field identifier
L:84 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:8 SEQ:5
L:91 M:283 W: Missing Blank Line separator, <400> field identifier
L:92 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:8 SEQ:6
L:99 M:283 W: Missing Blank Line separator, <400> field identifier
L:100 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:8 SEQ:7
L:107 M:283 W: Missing Blank Line separator, <400> field identifier
L:108 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:7 SEQ:8
L:115 M:283 W: Missing Blank Line separator, <400> field identifier
L:116 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:7 SEQ:9
L:123 M:283 W: Missing Blank Line separator, <400> field identifier
L:126 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:158 SEQ:10
L:133 M:283 W: Missing Blank Line separator, <400> field identifier
L:136 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:158 SEQ:11
L:143 M:283 W: Missing Blank Line separator, <400> field identifier
L:144 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:12
L:151 M:283 W: Missing Blank Line separator, <400> field identifier
L:152 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:32 SEQ:13
L:159 M:283 W: Missing Blank Line separator, <400> field identifier